Figure 1(A)

```
GGATCGTCTCAGGTCAGCGGAGGGA     25
                SL33
GGAGACTTATAGACCTATCCAGTCT     50
TCAAGGTGCTCCAGAAAGCAGGAGT     75
TGAAGACCTGGGTGTGAGGGACACA    100
TACATCCTAAAAGCACCACAGCAGA    125
GGAGGCCCAGGCAGTGCCAGGAGTC    150
AAGGTTCCCAGAAGACAAACCCCCT    175
AGGAAGACAGGCGACCTGTGAGGCC    200
CTAGAGCACCACCTTAAGAGAAGAA    225
        SL34
GAGCTGTAAGCCGGCCTTTGTCAGA    250
GCCATCATGGGGGACAAGGATATGC    275
CTACTGCTGGGATGCCGAGTCTTCT    300
CCAGAGTTCCTCTGAGAGTCCTCAG    325
AGTTGTCCTGAGGGGGAGGACTCCC    350
AGTCCTCTCCAGATTCCCCAGAG     375
TTCTCCTGAGAGCGACGACACCCTG    400
TATCCTCTCCAGAGTCCTCAGAGTC    425
GTTCTGAGGGGGAGGACTCCTCGGA    450
TCCTCTCCAGAGACCTCCTGAGGGG    475
AAGGACTCCCAGTCTCCTCTCCAGA    500
TTCCCCAGAGTTCTCCTGAGGGCGA    525
CGACACCCAGTCTCCTCTCCAGAAT    550
TCTCAGAGTTCTCCTGAGGGGAAGG    575
ACTCCCTGTCTCCTCTAGAGATTTC    600
TCAGAGCCCTCCTGAGGGTGAGGAT    625
GTCCAGTCTCCTCTGCAGAATCCTG    650
CGAGTTCCTTCTTCTCCTCTGCTTT    675
ATTGAGTATTTTCCAGAGTTCCCCT    700
```

Figure 1(B)

```
GAGAGAACTCAGAGTACTTTTGAGG        725
GTTTTCCCCAGTCTCCTCTCCAGAT        750
TCCTGTGAGCTCCTCCTCCTCCTCC        775
ACTTTATTGAGTCTTTTCCAGAGTT        800
CCCCTGAGAGAACTCAGAGTACTTT        825
TGAGGGTTTTCCCCAGTCTCTTCTC        850
CAGATTCCTATGACCTCCTCCTTCT        875
CCTCTACTTTATTGAGTATTTTCCA        900
GAGTTCTCCTGAGAGTGCTCAAAGT        925
ACTTTTGAGGGTTTTCCCCAGTCTC        950
CTCTCCAGATTCCTGGGAGCCCCTC        975
CTTCTCCTCCACTTTACTGAGTCTT        1000
TTCCAGAGTTCCCCTGAGAGAACTC        1025
ACAGTACTTTTGAGGGTTTTCCCCA        1050
GTCTCCTCTCCAGATTCCTATGACC        1075
TCCTCCTTCTCCTCTACTTTATTGA        1100
GTATTTTCCAGAGTTCTCCTGAGAG        1125
TGCTCAAAGTACTTTTGAGGGTTTT        1150
CCCCAGTCTCCTCTCCAGATTCCTG        1175
GGAGCCCCTCCTTCTCCTCCACTTT        1200
ACTGAGTCTTTTCCAGAGTTCCCCT        1225
GAGAGAACTCACAGTACTTTTGAGG        1250
GTTTTCCCCAGTCTCCTCTCCAGAT        1275
TCCTATGACCTCCTCCTTCTCCTCT        1300
ACTTTATTGAGTATTTTACAGAGTT        1325
CTCCTGAGAGTGCTCAAAGTGCTTT        1350
TGAGGGTTTTCCCCAGTCTCCTCTC        1375
CAGATTCCTGTGAGCTCCTCTTTCT        1400
```

Figure 1(C)

```
CCTACACTTTATTGAGTCTTTTCCA    1425
GAGTTCCCCTGAGAGAACTCAGAGT    1450
ACTTTTGAGGGTTTTCCCCAGTCTC    1475
CTCTCCAGATTCCTGTGAGCTCCTC    1500
CTCCTCCTCCTCCACTTTATTGAGT    1525
CTTTTCCAGAGTTCCCCTGAGTGTA    1550
CTCAAAGTACTTTTGAGGGTTTTCC    1575
CCAGTCTCCTCTCCAGATTCCTCAG    1600
AGTCCTCCTGAAGGGGAGAATACCC    1625
ATTCTCCTCTCCAGATTGTTCCAAG    1650
TCTTCCTGAGTGGGAGGACTCCCTG    1675
TCTCCTCACTACTTTCCTCAGAGCC    1700
CTCCTCAGGGGGAGGACTCCCTATC    1725
TCCTCACTACTTTCCTCAGAGCCCT    1750
CCTCAGGGGGAGGACTCCCTGTCTC    1775
CTCACTACTTTCCTCAGAGCCCTCA    1800
GGGGGAGGACTCCCTGTCTCCTCAC    1825
TACTTTCCTCAGAGCCCTCCTCAGG    1850
GGGAGGACTCCATGTCTCCTCTCTA    1875
CTTTCCTCAGAGTCCTCTTCAGGGG    1900
GAGGAATTCCAGTCTTCTCTCCAGA    1925
GCCCTGTGAGCATCTGCTCCTCCTC    1950
CACTCCATCCAGTCTTCCCCAGAGT    1975
TTCCCTGAGAGTTCTCAGAGTCCTC    2000
CTGAGGGGCCTGTCCAGTCTCCTCT    2025
CCATAGTCCTCAGAGCCCTCCTGAG    2050
GGGATGCACTCCCAATCTCCTCTCC    2075
AGAGTCCTGAGAGTGCTCCTGAGGG    2100
```

Figure 1(D)

```
GGAGGATTCCCTGTCTCCTCTCCAA        2125
ATTCCTCAGAGTCCTCTTGAGGGAG        2150
AGGACTCCCTGTCTTCTCTCCATTT        2175
TCCTCAGAGTCCTCCTGAGTGGGAG        2200
GACTCCCTCTCTCCTCTCCACTTTC        2225
CTCAGTTTCCTCCTCAGGGGGAGGA        2250
CTTCCAGTCTTCTCTCCAGAGTCCT        2275
GTGAGTATCTGCTCCTCCTCCACTT        2300
CTTTGAGTCTTCCCAGAGTTTCCC         2325
TGAGAGTCCTCAGAGTCCTCCTGAG        2350
GGGCCTGCTCAGTCTCCTCTCCAGA        2375
GACCTGTCAGCTCCTTCTTCTCCTA        2400
CACTTTAGCGAGTCTTCTCCAAAGT        2425
TCCCATGAGAGTCCTCAGAGTCCTC        2450
CTGAGGGGCCTGCCCAGTCTCCTCT        2475
CCAGAGTCCTGTGAGCTCCTTCCCC        2500
TCCTCCACTTCATCGAGTCTTTCCC        2525
AGAGTTCTCCTGTGAGCTCCTTCCC        2550
CTCCTCCACTTCATCGAGTCTTTCC        2575
AAGAGTTCCCCTGAGAGTCCTCTCC        2600
AGAGTCCTGT**GATC**TCCTTCTCCTC    2625
CTCCACTTCATTGAGCCCATTCAGT        2650
GAAGAGTCCAGCAGC<u>CCAGTAGATG</u>  2675
                SL26
<u>AATATACAAGTT</u>CCTCAGACACCTT   2700
GCTAGAGAGTGATTCCTTGACAGAC        2725
AGCGAGTCCTTGATAGAGAGCGAGC        2750
CCTTGTTCACTTATACACTGGATGA        2775
AAAGGTGGACGAGTTGGCGCGGTTT        2800
```

Figure 1(E)

CTTCTCCTCAAATATCAAGTGAAGC   2825
      SL27
AGCCTATCACAAAGGCAGAGATGCT   2850
GACGAATGTCATCAGCAGGTACACG   2875
GGCTACTTTCCTGT*GATC*TTCAGGA   2900
AAGCCCGTGAGTTCATAGAGATACT   2925
TTTTGGCATTTCCCTGAGAGAAGTG   2950
GACCCTGATGACTCCTATGTCTTTG   2975
TAAACACATTAGACCTCACCTCTGA   3000
GGGGTGTCTGAGTGATGAGCAGGGC   3025
ATGTCCCAGAACCGCCTCCTGATTC   3050
TTATTCTGAGTATCATCTTCATAAA   3075
GGGCACCTATGCCTCTGAGGAGGTC   3100
ATCTGGGATGTGCTGAGTGGAATAG   3125
GGGTGCGTGCTGGGAGGGAGCACTT   3150
TGCCTTTGGGGAGCCCAGGGAGCTC   3175
CTCACTAAAGTTTGGGTGCAGGAAC   3200
ATTACCTAGAGTACCGGGAGGTGCC   3225
CAACTCTTCTCCTCCTCGTTACGAA   3250
TTCCTGTGGGGTCCAAGAGCTCATT   3275
CAGAAGTCATTAAGAGGAAAGTAGT   3300
AGAGTTTTTGGCCATGCTAAAGAAT   3325
ACCGTCCCTATTACCTTTCCATCCT   3350
CTTACAAGGATGCTTTGAAAGATGT   3375
GGAAGAGAGAGCCCAGGCCATAATT   3400
GACACCACAGATGATTCGACTGCCA   3425
CAGAAAGTGCAAGCTCCAGTGTCAT   3450
GTCCCCCAGCTTCTCTTC**TGA**GTGA   3475
AGTCTAGGGCAGATTCTTCCCTCTG   3500

Figure 1(F)

```
AGTTTGAAGGGGGCAGTCGAGTTTC    3525
TACGTGGTGGAGGGCCTGGTTGAGG    3550
CTGGAGAGAACACAGTGCTATTTGC    3575
ATTTCTGTTCCATATGGGTAGTTAT    3600
GGGGTTTACCTGTTTTACTTTTGGG    3625
TATTTTTCAAATGCTTTTCCTATTA    3650
ATAACAGGTTTAAATAGCTTCAGAA    3675
TCCTAGTTTATGCACATGAGTCGCA    3700
CATGTATTGCTGTTTTTCTGGTTTA    3725
AGAGTAACAGTTTGATATTTTGTAA    3750
AAACAAAAACACACCCAAACACACC    3775
ACATTGGGAAAACCTTCTGCCTCAT    3800
TTTGTGATGTGTCACAGGTTAATGT    3825
GGTGTTACTGTAGGAATTTTCTTGA    3850
AACTGTGAAGGAACTCTGCAGTTAA    3875
ATAGTGGAATAAAGTAAAGGATTGT    3900
TAATGTTTGCATTTCCTCAGGTCCT    3925
TTAGTCTGTTGTTCTTGAAAACTAA    3950
AGATACATACCTGGTTTGCTTGGCT    3975
TACGTAAGAAAGTAGAAGAAAGTAA    4000
ACTGTAATAAATAAAAAAAAAAAAA    4025
AAAAAA                       4031
```

FIG. 2(A)

```
A1  [exon I]
A1  CCATTCTGAGGGACGGCGTA GAGTTCGGCCGCGAAGGAACCT GACCCAGGCTCTGTGAGGAG GCAAG|exon II           GGATCGT  CTCAGGTCAGCGCGGAGGGAGG   27
C1  .....................................................................        intron I  |exon I
C1  ...........................................................................................................................

A1  ..............................................//ctg gagctccaggaaccaggcag tgaggccttggt------c  tgagacagtatcctcaggtc
A1  AGACTTATAGACCTATCCAG TCTTCAAG|gt//.....//cag |GTGCTCCAGAAAGCAGGAGT TGAAGACCTGGGTGTGTGAGGG ACACATACATCCTAAAAGCA   115
C1  exon I|  intron I  |exon II

A1  acagagagaggaggatgcacag ggtgtgccagcagtgaatgt tt-----gccctgaatgca caccaaggggcccacctgcc acaggacacataggactca
A1  CCACAGAGAGGAGGCCCAG GCAGTGCCAGGAGTCAAG|gt gagtgcacgacctgactgtg taccaagggccgtacccca  gaaacagtgtcagacctggc   70
C1  exon II|            intron II

A1  cagagtctggcctcacctcc ctactgtcagtcctgtagaa tcgac-ctctgctggccggc tgtacccctga-gtacccct cacttcctccttcag|GTTTT
A1  agcaccggccctgtagccac ccactgtcattcctggtgcc  gtgtgcccgagggtgcttct cgcgtccttctacag|GTTCC                    158
C1                                                           intron II|exon III

A1  ggttcag--ttctcagctgag gcctctcacacactccctct ctccc-cag|CCTGTGTGGGTC TTCATTG-CCCAGCTCCTGC CCACACTCCTGCCCTGCTGCC   188
C1  G|G|gtgttctcagctgag gccactggcactgtccctct ctccctcagtcctgtgggat cccatcatacctattcgtgt tcacacgttacctgctgct
C1  exon III|G| intron III                          intron III|exon III

A1  CAGGGGGACAGGCCAACCCAG AGGACAGGATTCCCTGGAGG CCACAGAGAGGAGGCACC----A AGGAGAAGATCT|gtaagtag gcctttgttagagtctccaa
A1  CAGAAGACAAACCCCCTAGG AAGACAGGCGACCTGTGAGG CCCTAGAGCAGCACCACCTTAAG AGAAGAAGAGCTGTAAGCCG GCCTTTGTGTCAGAGCCATCAT   258
C1  M                                                                            exon II|intron II

A1                                                          M                                                          1
C1

A1  CT--GACGAGAGTCATCATG TCTCTTGAGCAGAGGAGTCT GCACTGCAAGCCTGAGGAAG CCCTTGAGGCCCAACAAGAG GCCCTGGGCCTGGTGTGTGT   286
A1        M   S  L  E  Q  R  S  L  H  C  K  P  E  E  A  L  E  A  Q  Q  E  A  L  G  L  V  C  V
C1  cctgaacaatatcatcatg cctctcttctaaaccttcc acgcccagcttgagcaag gcttccagaaggcaatttc atactggagttggtagatgc

A1  GCAGGCTGCGCCACCTCCTCCT CCTCTCCTCTGGTCCTGGGC ACCCTGGAGGAGGTGCCCAC TGCTGGGTCAACAGATCCTC CCCAGAGTCCTCAGGGGAGCC   386
A1   Q  A  A  T  S  S  S  P  L  V  L  G  T  L  E  E  V  P  T  A  G  S  T  D  P  P  Q  S  P  Q  G  A
C1  agaggatccccca--------                                               ------gatgaggaagaggag gaagcttcctccattttctc

A1  TCCGGCCTTTCCCCACTACCAT CAACTTCACTCGACAGAGGC AACCC-----   431
A1   S  A  F  P  T  T  I  N  F  T  R  Q  R  Q  P
C1  .......................................... ....... ....  ttcctctcttccactttttat
```

FIG. 2(B)

```
C1  tcccctcgtcctcctcctgt ttttcttctcatcctcatc ctcctctctgcttctgcgtt ctccag GGGACAAAGGATATG CCTACTGCTGGGGATGCCGAG    13
                                                              intron III |  D   K   D   M   P   T   A   G   M   P   S
                                                                    exon IV

A1  ................................................................................................................   294
C1  TCTTCTCCAGAGAGTTCCTCTG AGAGTCCTCAGAGTTGTCCT GAGGGGGGGAGGAGGACTCCCAGTC TCCTCTCCAGAGATTCCCCCAGA GTTCTCCTGAGAGCGGACGAC   394
    L  L  Q  S  S  E     S  P  Q  S |Y  P  E  G  E  D  S  Q  S  P  L  Q  I|P|Q  S     S  P  E  S  D  D     46

A1  ................................................................................................................   494
C1  ACCCTGTATCCTCTCCAGAG TCCTCAGAGTCGTCGTTCTGAGG GGGAGGAGGACTCCTCGGAGTCCT CTCCAGAGAGACCTCCTGAGGGG GAAGGGACTCCCAGTGTCTCCTC   80
    T  L  Y  P  L  Q  S |P|Q  S  R  S  E  G  E  D  S  S  D  P  L  Q  R|P  P  E  G  K  D  S  Q  S  P  L  C

A1  ................................................................................................................   594
C1  TCCAGGATTCCCCCAGAGTTCT CCTGAGGGGCGGACGAGCACCCA GTCTCCTCCAGAGAATCCTC AGAGTTCTCCTGAGGGGGAAG GACTCCCTGTCTCCTCTAGA   113
    Q  I  P |Q  S  S  P  E  G  D  D  T  Q  S  P  L  Q  N  S| Q  S  S  P  E  G  K  D  S  L  S  P  L  E

A1  ................................................................................................................   694
C1  GATTTCTCAGAGAGCCCTCCTG AGGGTGAGGAGGATGTCCAGTCT CCTCTGCAGAATCCTGCGAG TTCCTTCTTCTTCTCCTGCTT TATTGAGTAGTATTTCCAGAGT   146
    I  S| Q  S  P  P  E  G  E  D  V  Q  S  P  L  Q  N|P|A|S  F  F  S  S  A  L  L  S  I  F  Q  S

A1  ................................................................................................................   794
C1  TCCCCTGAGAGTATTCAAAG TCCTTTTGAGGGTTTTCCCC AGTCTGTTCTCCAGATTCCT GTGAGCGCGCCGCCTCCCTC CACTTTAGTGAGTATTTTCC   180
    S  P  E  S| Q| S  P  F  E  G  F  P  Q  S  V  L  Q  I  P |V  S  A  A  S  S  T  L  V  S  I  F  Q

A1  AGAGTCCCCTGAGAGTACT CAAAGTCCTTTGAGGGGTTT TCCCCAGTCCTCCACTCCAGA TTCCTGTGAGGCCGGCGTCCCTTC TCCTCCACTTTATTGAGTAT   894
C1  S  P  E  S  T | Q| S  P  F  E  G  F  P  Q  I  P |V  S  R  S  F  S  S  T  L  S  I   213

A1  TTTCCAGAGTTCCCCTGAGA GAAGTCAGAGAGAACTTCTGAG GGTTTTGCACAGTCTCCCTCT CCAGATTCCTGTGTGAGCTCCT CCTCGTGTCCTCCACTTTACTG   994
    F Q| S  S  P  E  R  S  Q| R  T  S  E  G  F  A  Q  S  P  L  Q  I  P|V  S  S  S  S  S  T  L  L   246
```

FIG. 2(C)

```
A1  ..........................................................................
C1  AGTCTCTTTCCAGAGTCCCC TGAGAGAACTCAGAGTACTT TTGAGGGTTTTCCCCAGTCT CCACTCCAGATTCCTGTGAG CCGGCTCCTTCCTTCTCCTCCCACTT 1094
A1   S _ L _ F _ Q _ S _ S _ P _ E _ R _ T _ Q | S _ T _ F _ E _ G _ F _ P _ Q _ S _ P _ L _ Q _ I _ P | V _ S _ R _ S _ F _ S _ S _ T _ L

A1  ..........................................................................
C1  TATTGAGTAGTATTTTCCAGAGT TCCCCTGAGAGAACTCAGAG TACTTTTGAGGGGTTTTGCCC AGTCTCCTCTCCAGATTCCT GTGAGCTCCTTCCTTCTCCTCCTC 1194
A1   _ L _ S _ I _ F _ Q _ S _ S _ P _ E _ R _ T _ Q | S _ T _ F _ E _ G _ F _ A _ Q _ S _ P _ L _ Q _ I _ P | V _ S _ S _ S _ S _ S _ S

A1  ..........................................................................
C1  CACTTTATTGAGTAGTCTTTTCC AGAGTTCCCCTGAGAGAACT CAGAGTACTTTTGAGGGGTTT TCCCCAGTCTCCTCTCCTCCAGA TTCCTATGACCTCCTCCTTC 1294
A1   _ T _ L _ L _ S _ L _ F _ Q _ S _ S _ P _ E _ R _ T _ Q | S _ T _ F _ E _ G _ F _ P _ Q _ S _ L _ L _ Q _ I _ P | M _ T _ S _ S _ F

A1  ..........................................................................
C1  TCCCTCTACTTTATTGAGTAT TTTCCAGAGTCTCCTGAGA GTGCTCAAAGTACTTTTGAG GGTTTCCCCAGTCTCCTCCT CCAGATTCCTGGGAGCCCCT 1394
A1   S _ S _ T _ L _ L _ S _ L _ F _ Q _ S _ S _ P _ E _ S _ A _ Q | S _ T _ F _ E _ G _ F _ P _ Q _ S _ P _ L _ Q _ I _ P | G _ S _ P _ S

A1  ..........................................................................
C1  CCTTCTCCTCCTCCCACTTTACTG TATTGAGTAGTATTTTACAGAGT TCTCCTGAGAGTGCTCAAAG TGCTTTTGAGGGGTTTTCCCC AGTCTCCTCCAGATTCCT 1494
A1   _ F _ S _ S _ T _ L _ L _ S _ L _ F _ Q _ S _ P _ E _ R _ T _ H | S _ T _ F _ E _ G _ F _ P _ Q _ S _ P _ L _ Q _ I _ P | M _ T

A1  ..........................................................................
C1  CTCCCTCCTTCTCCTCTACTT CACTTTATTGAGTAGTCTTTTCC AGAGTTCCCCTGAGAGAACT CAGAGTACTTTTGAGGGGTTT TCCCCAGTCTCCTCTCCTCCAGA 1594
A1   _ S _ F _ S _ S _ T _ L _ L _ S _ L _ F _ Q _ S _ S _ P _ E _ R _ Q | S _ A _ F _ E _ G _ F _ P _ Q _ S _ P _ L _ Q _ I _ P

A1  ..........................................................................
C1  GTGAGCTCCTCCTTCTCCTA CACTTTATTGAGTAGTCTTTTCC AGAGTTCCCCTGAGAGAACT CAGAGTACTTTTGAGGGGTTT TCCCCAGTCTCCTCTCCTCCAGA 1694
A1  V _ S _ S _ F _ S _ Y _ T _ L _ L _ S _ L _ F _ Q _ S _ S _ P _ E _ R _ T _ Q | S _ T _ F _ E _ G _ F _ P _ Q _ S _ P _ L _ Q

A1  ..........................................................................
C1  TTCCTGTGTGAGCTCCTCCTCC TCCTCCTCCTCCACTTTATTGAG TCTTTTCCAGAGTCCCCTG AGTGTACTCAAAGTACTTTT GAGGGTTTTCCCCAGTCTCC 1794
A1  P | V _ S _ S _ S _ S _ S _ S _ T _ L _ L _ S _ L _ F _ Q _ S _ S _ P _ E _ C _ T _ Q | S _ T _ F _ E _ G _ F _ P _ Q _ S _ P 513
```

```
A1  280
C1  313
A1  313
```

FIG. 2(D)

A1 ......
C1 TCTCCCAGATTCCTCAGAGAGTC CTCCTGAAGGGGGAGAATACC CATTCTCCTCCTCCAGATTGT TCCAAGTCTTCCTGAGTGGG AGGACTCCCCTGTCTCCTCAC 1894
   L Q I P Q S P E G E N T H S P L Q I V P S L P E W E D S L S P H 546

A1 ......
C1 TACTTTCCTCAGAGAGCCCTCC TCAGGGGGGAGGAGGACTCCCTAT CTCCTCACTACTTTCCTCAG AGCCCCTCCAGGGGGGAGGAGGA CTCCCTGTCTCCTCACTACT 1994
   Y F P Q S P P Q G E D S L S P H Y F P Q S P P Q G E D S L S P H Y F 580

A1 ......
C1 TTCCCTCAGAGCCCCTCAGGGGG GAGGACCCCGTGTCTCCTCA CTACTTTCCTCAGAGAGCCCCTC CTCAGGGGGGAGGAGGACTCCATG TCTCCTCTCTCCTACTTTCCTCA 2094
   F P Q S P Q G E D S L S P H Y F P Q S P Q G E D S M S P L Y F P Q 613

A1 ......
C1 GAGTCCCTCTTCAGGGGGGGAGG AATTCCAAGTCTTCTCTCCAG AGCCCTCCACTCCCAGTC TTCCCAGAGAGTTCCCTGAG 2194
   S P L Q G E F Q S S L Q S P V S I C S S S T P S S L P Q S F P E 646

A1 ......
C1 AGTTCTCTCAGAGAGTCCCTGA GGGGGCCTGTCGTCCAGTCTCCTC TCCATAGTCGTCCTCAGAGAGCCCT CCTGAGGGGGGATGCACTCCCA ATCTCCTCTCCAGAGAGTCCTG 2294
   S S Q S P P E G P V Q S P L H S P Q S P E G M H S Q S P L Q S P E 680

A1 ......
C1 AGAGGTGCTCCTGAGGGGGGAG GATTCCCTGTCTCCTCTCCA AATTCCTCAGAGAGTCCCTCTTG AGGGAGGAGGACTCCCCTGTCT TCTCTCCATTTTCCTCAGAG 2394
   S A P E G E D S L S P L Q I P S P L E G E D S L S L H F P Q S 713

A1 ......
C1 TCCCTCCTGAGTTGGGGGAGGACT CCCTCTCCTCCTCCACTTT CCTCAGTTTCCTCCTCAGGG GGAGGACTTCCAGTCTCTCTC TCCAGAGTCGTCCTGTTGAGTATC 2494
   P P E W E D S L S P L H F P Q F P P Q G E D F Q S S L Q S P V S I 746

A1 ......
C1 TGCTCCTCCTCCACTTCTT GAGTCGTCTTCCCCCAGAGTTTCC CTGAGAGTGCCTCAGAGTC CCTGAGGGGGGCCTGCTGCCA CAGTCTCCTCAGAGTCCCTGTCA 2594
   C S S S T S L S L P Q S F P E S P Q S P E G P L Q R P V S 780

A1 ......
C1 GCTCCTCTTCTTCCTCTACACT TTAGGCGAGTCTCTTCTCCAAAG TTCCCATGAGAGAGTCCTCAGA GTCCTCCTGAGGGGGGCCTGCC CAGTCTCCTCAGAGAGTCC 2694
   S F F S Y T L A S L L Q S S H E S P Q S P E G P A Q S P L Q S P 813

FIG. 2(E)

```
A1    ..............................................................................................................
C1    TGTGAGCTCCTTCCCCCTCCT CCACTTCATCGAGAGTCTTTCC CAGAGTTCTCCTGTGAGCTC CTTCCCCTCCTCCCCACTTCAT CGAGTCTTCCAAGAGTTCC .......      2794
      [ V  S  S  F  P  S  S _ _  _ _ T _ S  S  L  S _ _ _  _ _ S  S _ _ Q  S  S                                                    846

A1    ..............................................................................................................
C1    CCTGAGAGTCCTTCTCCCAGAG TCCTGTGATCTCCTCTCCT CCTCCACTTCATTGAGCCCA TTCAGTGAAGAGTCCAGCAG CCCAGTAGATGAATATACAA       2894
      P  E  S  P  L  Q  S [ V  _ I  S  F  S  S _ _ S  T  S  L  S  P  _ S ] S  E  E  S  S  P  V  D  E  Y  T  S            468
                         [ V _ I _ _ S  F  S  S _ _ S  T  S  L  S  P  _ S ] S  E  E  S  S  P  V  D  E  Y  T  S            89

A1    GCACCTCTTGTATCCTG.........................................  AGTGAGGGTTCCAGCAG CCGTGAAGAGAGGAGGGGCCAA          2994
      T  S  C  I  L  .  .  .  .  .  .  .  .  .  .  .  .          S  E  G  S  S  S  R  E  E  E  G  P  S                  523
C1    GTTCCTCAGACACCTTGCTA GAGAGTGATTCCTTGACAGA CAGCGAGTCCTTGATAGAGA GCGAGCCCCTTGTTCACTTAT ACACCTGGATGAAAAGGTGGA      108

A1    TGATTTGGTTGGTTTTCTGC TCCTCAAATATCGAGCCAGG GAGGCCAGTCACAAAGGCAGA AATGCTGGAGAGTGTCATCA AAAATTACAAGCACTGTTTT      3094
      D  L  V  G  F  L  L  L  K  Y  R  A  R  E  P  V  T  K  A  E  M  L  E  S  V  I  K  N  Y  K  H  C  F               623
C1    CGAGTTGGGCGCGGTTTCTTC TCCTCAAATCAAGTGAAG CAGCCTATCACAAAGGCAGA GATGCTGACGAATGTCATCA GCAGGTACACGGGCTACTTT       140

A1    DLVGFLLL KYRAR EPVTKAE MLESVIK        E  S  L  F  R  A  V  I  T  K  K  V  A                      3191
      E  L  A  R  F  L  L  L  K  Y  Q  V  K  Q  P  I  T  K  A  E  M  L  T  N  V  I  S  R  Y  T  G  Y  F               913
C1    .....................  GAGGTCCTTGTTCCGAGCA GTAATCACTAAGAAGGTGGC                                                946

A1    PEIFGKA SESLQLV FGIDVK EADPTGH SYVLVTC                                                           174
      P  E  I  F  G  K  A  R  E  F  I  E  I  L  F  G  I  S  L  R  E  V  D  P  -  D  D  S  Y  V  F  V  N  T          979
C1    CCTGAGATCTTCGGGCAAAGC CTCTGAGTCCTTGCAGCTGG TCTTTGGCATTGACGTGAAG GAAGCAGACCCCACCGGCCA CTCCTATGTCTTTGTAAACA       723

A1    PVIFRKA REFIEIL FGISLR EVDP-DD SYVFVNT                                                           3291
      L  G  L  S  Y  D  G  L  L  G  D  N  Q  I  M  P  K  T  G  F  L  I  I  V  L  V  M  I  A  M  E  G  G            823
C1    CATTAGACCTCACCTCTGAG GGGTGTCGAGTGATGAGCA GATCAATGCCCAAGACAGGCT ATGATTGCAATGGAGGGCGG                           207

A1    LGLSYD GLLGDNQ IMPKTGF LIIVLV MIAMEGG                                                            3391
      L  D  L  T  S  E  G  C  L  S  D  E  Q  G  M  S  Q  N  R  L  L  I  L  S                                      1012
C1    GCCTAGGTCTCCTCCTATGAT GGCCTGCTGCTGGGTGTAATCA GATCATGCCCAAGACACAGGCT TCCTGATTCTTATTCTGAGT                      823

A1    HAPEEEI WEELSF MEVYDGR EHSAYGE PRKLLT                                                            240
      Y  A  S  E  E  V  I  W  D  V  L  S  G  I  G  V  R  A  G  R  E  H  F  A  F  G  E  P  R  E  L  L  T          923
C1    CCATGCTCCTGAGGAGGAAA TCTGGGAGGAGGAGCTGAGTGTG ATGGAGGTGTATGATGGGAG GGAGCACAGTGCCTATGGGG AGCCCAGGGAGCTGCTCACC     1045
```

FIG. 2(F)

```
         Q  D  L  V  Q  E  K  Y  L  E  Y  R  Q  V     P  D  S  D  P  A     R  Y  E  F  L  W  G     P  R  A  L  A  E  T        274
A1  CAAGATTTGGTGCAGGAAAA  GTACCTGGAGTACCGGCAGG  TGCCGGACAGTGATCCCGCA  CGCCTATGAGAGTTCCTGTGTGGGG  TCCAAGGGGGCCCTCGCGCTGAAA   1023
C1  AAAGTTTGGGTGCAGGAACA  TTACCTAGAGTACCGGGAGG  TGCCCAACTCTCCTCCCCCT  CGTTACGGAATTCCTGTGTGGGGG  TCCAAGAGCTCATTCAGAAG        3491
         K  V  W  V  Q  E  H  Y  L  E  Y  R  E  V     P  N  S  S  P  P     R  Y  E  F  L  W  G     P  R  A  H  S  E  V        1079

         S  Y  V  K  V  L  E  Y  V  I  K  V  S     A  R  V  R  F  F  F     P  S  L  R  E  A     L  R  E  E  E              307
A1  CCAGCTATGTGAAAGTCCTT  GAGTATGTGATCAAGGTCAG  TGCAAGAGTTCGGCTTTTTCT  TCCCATCCCTGCGTGAAGCA  GCTTTGAGAGAGGAGGAAGA         1123
C1  TCATTAAGAGGAAAGTAGTA  GAGTTTTTGGCCATGCTAAA  TTCCATCCTCTTACAAGGAT  GCTTTGAAAGATGTGGAAGA                               3591
         I  K  R  V  V  E  F  L  A  M  L  K  N  T  V  P  I  T  F  P  S  S  Y  K  D  A  L  K  D  V  E  E                       1112

         G  V  OPA                                                                                                           309
A1  GGGAGAGTCTGAGCATGAGTTG  CAGCCAAGGCCGGTCAGTG  GGGACTGGGCCAGTGCCACCT  TCCAGGGGGCCGTCCCAGCAG  CTTCCCCTGCCTCGTGTGAC       1223
C1  GAGAGCCCAGGCCATAATTG  ACACCACAGATGATTCGACT  GCCACAGAAAGTGCAAGCTC  CAGTGTCATGTCCCCAGCT  TCTCTTCTGAGTGAAGTCTA         3691
         R  A  Q  A  I  I  D  T  T  D  D  S  T  A  T  E  S  A  S  S  S  V  M  S  P  S  F  S  S  E  OPA                       1142

A1  ---ATGAGGGCCCATTCTTCTTCA  CTCTGAAGAGAGCGGTCAGT  GTTCTCAGTAGTAG-  .............  GTTTC                                  1279
C1  GGGCAGAGTTCTTCCCTCTGA  GTTTGAAGGGGGGCCAGTCGAG  TTTCTACGTGGTGGAGGGGCC  TGGTTGAGGCTGGAGAGAAC  ACAGTGCTATTTGCAATTCT     3791

A1  TGTTCTATTGGGGTGACTTGG  AGATTTATCTTTGTTCTCTT  TT--TTTTAGGGGATGGTTG  AATGAACTTCAGCGATCCAAG                              1377
C1  GTTCCCATATGGGTAGTTATG  GGGTTTACCTGTTTTACTTT  TTCCTATTAATAACAGGTTT  AAATAGCTTCAGAATCCTAG                               3891

A1  TTTATGAATGACAGCAGT-C  ACACAGTGTCTGTGTGTATAG  TTTAAGGGTAAGAGTGTCTGT  GTTTTATTCAGATTGGGAAA  TCCATTCTATTTTGTGAATT        1476
C1  TTTATGCACATGAGTCGCAC  ATGTATTGCTGTGTTTTCTGG  TTTAAGAGTAACAGTTGAT  ATTTTGTAAAACAAAAACA  CACCCAAACACACCACATTG          3991

A1  GGGGATAATAAACAGCAGTGGA  ATAAGTACTTAGAAATGTGA  AAAATGAGGAGCAGTAAAATAGA  TGAGATAAAGAGAACTAAAGAA  ATTAAGAGATAGTCAATTCT    1576
C1  GGAAAACCTTCTGCCTCATT  TTGTGATGTGTCACAGGTTA  TTTTCTTGAAACTGTGAAGG  AACTCTGCAGTTAAATAGTG                               4091

A1  TGCCTTATACCTCAGTCTAT  TCTGTAAAATTTTTAAAGAT  ATATGCATACCTGGATTCC  TTGGCTCTCTTTGAGAATGTA  AGAGAAATTAAATCTGAATA          1676
C1  GAATAAAGTAAAGGATTGTT  AATGTTTGCATTCCTCTCAGG  TCCTTTAGTCTGTGTGTTCTT  GAAAACTAAAGAATACATACC  TGGTTTGCTTGGCTTACGTA       4191

A1  AAGAATTCTTCCTTGT----  .............----                                                                               1691
C1  AGAAAGTAGAAGAAAGTAAA  CTGTAATAAATAAA                                                                                   4225
```
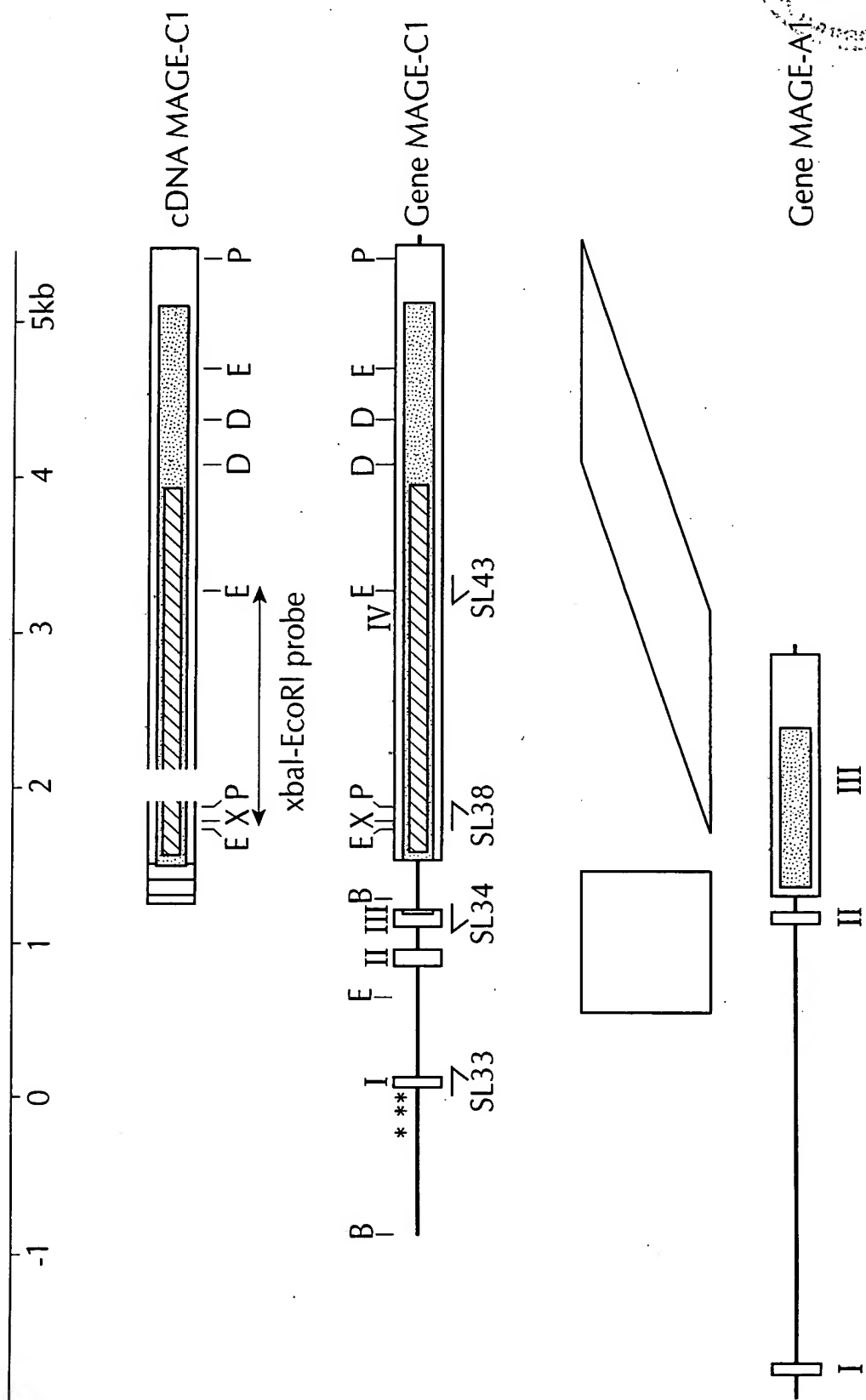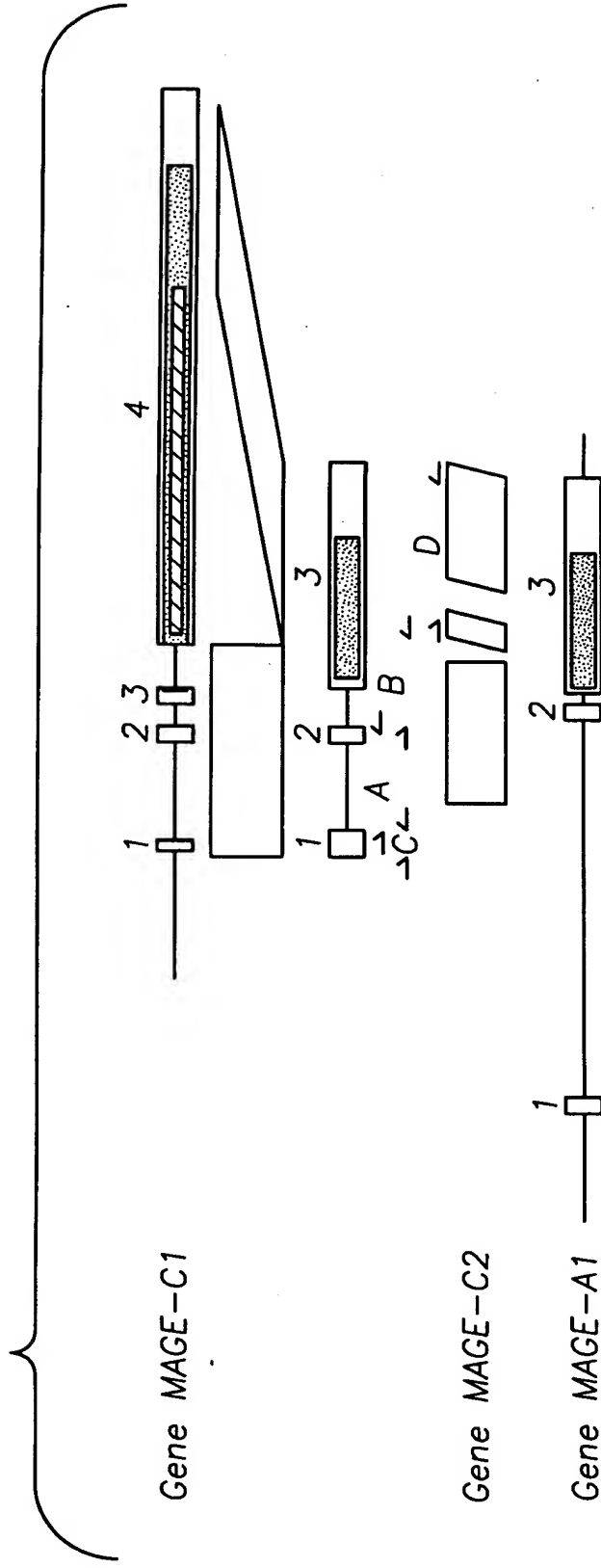
FIG. 3

FIG.4

Gene MAGE-C1

Gene MAGE-C2

Gene MAGE-A1

Figure 5   Nucleotide sequence of gene MAGE-C3

(SEQ ID NO: 21)

The sequence corresponds to nucleotides 3761 to 4801 of PAC clone 232G24 (GenBank accession number AL022152). It has been renumbered in this figure, taking as nucleotide number 1 the first nucleotide of the start codon.

Primers SL164 and SL165 that were used in the RT-PCR assay are indicated.

```
ATGCCTCTCTTTCCAAACCTTCCACGCCTCAGCTTTGAGGAAGACTTCCA      50

GAACCCGAGTGTGACAGAGGACTTGGTAGATGCACAGGATTCCATAGATG     100

AGGAGGAGGAGGATGCCTCCTCCACTTCCTCTTCCTCTTTCCACTTTTTA     150

TTCCCCTCCTCCTCTTCCTTGTCCTCATCCTCACCCTTGTCCTCACCCTT     200
                          SL164
ACCCTCTACTCTCATTCTGGGTGTTCCAGAAGATGAGGATATGCCTGCTG     250

CTGGGATGCCACCTCTTCCCCAGAGTCCTCCTGAGATTCCTCCCCAGGGT     300

CCTCCCAAGATCTCTCCCCAGGGTCCTCCGCAGAGTCCTCCCCAGAGTCC     350

TCTAGACTCCTGCTCATCCCCTCTTTTGTGGACCCGATTGGATGAGGAGT     400

CCAGCAGTGAAGAGGAGGATACAGCTACTTGGCATGCCTTGCCAGAAAGT     450

GAATCCTTGCCCAGGTATGCCCTGGATGAAAAGGTGGCTGAGTTGGTGCA     500

GTTTCTTCTCCTCAAATATCAAACAAAAGAGCCTGTCACAAAGGCAGAGA     550

TGCTGACGACTGTCATCAAGAAGTATAAGGACTATTTTCCCATGATCTTC     600

GGGAAAGCCCATGAGTTCATAGAGCTAATTTTTGGCATTGCCCTGACTGA     650

TATGGACCCCGACAACCACTCCTATTTCTTTGAAGACACATTAGACCTCA     700

CCTATGAGGGAAGCCTGATTGATGACCAGGGCATGCCCAAGAACTGTCTC     750
                SL165
CTGATTCTTATTCTCAGTATGATCTTCATAAAGGGCAGCTGTGTCCCCGA     800

GGAGGTCATCTGGGAAGTGTTGAGTGCAATAGGGGTGTGTGCTGGGAGGG     850

AGCACTTTATATATGGGGATCCCAGAAAGCTGCTCACTATACATTGGGTG     900

CAGAGAAAGTACCTGGAGTACCGGGAGGTGCCCAACAGTGCTCCTCCACG     950

TTATGAATTTTTGTGGGGTCCAAGAGCCCATTCAGAGGCCAGCAAGAGAA    1000

GTCTTAGAGTTTTTATCCAAGCTATCCAGTATCATCCCTAG            1041
```

Figure 6   Amino-acid sequence of the putative MAGE-C3 protein   (SEQ ID NO: 22)

```
MPLFPNLPRLSFEEDFQNPSVTEDLVDAQDSIDEEEEDASSTSSSSFHFL      50
FPSSSSLSSSSPLSSPLPSTLILGVPEDEDMPAAGMPPLPQSPPEIPPQG     100
PPKISPQGPPQSPPQSPLDSCSSPLLWTRLDEESSSEEEDTATWHALPES     150
ESLPRYALDEKVAELVQFLLLKYQTKEPVTKAEMLTTVIKKYKDYFPMIF     200
GKAHEFIELIFGIALTDMDPDNHSYFFEDTLDLTYEGSLIDDQGMPKNCL     250
LILILSMIFIKGSCVPEEVIWEVLSAIGVCAGREHFIYGDPRKLLTIHWV     300
QRKYLEYREVPNSAPPRYEFLWGPRAHSEASKRSLRVFIQAIQYHP       346
```

**Figure 7   Nucleotide sequence of gene MAGE-B5
                (SEQ ID NO: 23)**

This sequence is the antiparallel sequence corresponding to nucleotides 123358 to 124185 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL189 and SL190 that were used in the RT-PCR assay are indicated.

```
ATGACTTCTGCAGGTGTTTTTAATGCAGGATCTGACGAAAGGGCTAACAG        50

TAGAGATGAGGAGTACCCATGTTCCTCAGAGGTCTCACCCTCCACTGAGA       100

GTTCATGCAGCAATTTCATAAATATTAAGGTGGGTTTGTTGGAGCAGTTC       150

CTGCTCTACAAGTTCAAAATGAAACAGCGTATTTTGAAGGAAGATATGCT       200

GAAGATTGTCAACCCAAGATACCAAAACCAGTTTGCTGAGATTCACAGAA       250

GAGCTTCTGAGCACATTGAGGTTGTCTTTGCAGTTGACTTGAAGGAAGTC       300

AACCCAACTTGTCACTTATATGACCTTGTCAGCAAGCTGAAACTCCCCAA       350

CAATGGGAGGATTCATGTTGGCAAAGTGTTACCCAAGACTGGTCTCCTCA       400
                        SL189
TGACTTTCCTGGTTGTGATCTTCCTGAAAGGCAACTGTGCCAACAAGGAA       450

GATACCTGGAAATTTCTGGATATGATGCAAATATATGATGGGAAGAAGTA       500

CTACATCTATGGAGAGCCCAGGAAGCTCATCACTCAGGATTTCGTGAGGC       550

TAACGTACCTGGAGTACCACCAGGTGCCCTGCAGTTATCCTGCACACTAT       600

CAATTCCTTTGGGGTCCAAGAGCCTATACTGAAACCAGCAAGATGAAAGT       650

CCTGGAATATTTGGCCAAGGTCAATGATATTGCTCCAGGTGCCTTCTCAT       700
                            SL190
CACAATATGAAGAGGCTTTGCAAGATGAGGAAGAGAGCCCAAGCCAGAGA       750

TGCAGCCGAAACTGGCACTACTGCAGTGGCCAAGACTGTCTCAGGGCGAA       800

GTTCAGCAGCTTCTCTCAACCCTATTGA                             828
```

Figure 8 **Amino-acid sequence of the putative MAGE-B5 protein (SEQ ID NO: 24)**

```
MTSAGVFNAGSDERANSRDEEYPCSSEVSPSTESSCSNFINIKVGLLEQF        50
LLYKFKMKQRILKEDMLKIVNPRYQNQFAEIHRRASEHIEVVFAVDLKEV       100
NPTCHLYDLVSKLKLPNNGRIHVGKVLPKTGLLMTFLVVIFLKGNCANKE       150
DTWKFLDMMQIYDGKKYYIYGEPRKLITQDFVRLTYLEYHQVPCSYPAHY       200
QFLWGPRAYTETSKMKVLEYLAKVNDIAPGAFSSQYEEALQDEEESPSQR       250
CSRNWHYCSGQDCLRAKFSSFSQPY                                275
```

Figure 9   **Nucleotide sequence of gene MAGE-B6**
(SEQ ID NO: 25)

This sequence is the antiparallel sequence corresponding to nucleotides 146417 to 147640 of BAC clone 46604 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL191 and SL192 that were used in the RT-PCR assay are indicated.

```
ATGCCTCGGGGTCACAAGAGTAAGCTCCGTACCTGTGAGAAACGCCAAGA          50

GACCAATGGTCAGCCACAGGGTCTCACGGGTCCCCAGGCCACTGCAGAGA         100

AGCAGGAAGAGTCCCACTCTTCCTCATCCTCTTCTCGCGCTTGTCTGGGT         150
                    SL191
GATTGTCGTAGGTCTTCTGATGCCTCCATTCCTCAGGAGTCTCAGGGAGT         200

GTCACCCACTGGGTCTCCTGATGCAGTTGTTTCATATTCAAAATCCGATG         250

TGGCTGCCAACGGCCAAGATGAGAAAAGTCCAAGCACCTCCCGTGATGCC         300

TCCGTTCCTCAGGAGTCTCAGGGAGCTTCACCCACTGGCTCTCCTGATGC         350

AGGTGTTTCAGGCTCAAAATATGATGTGGCTGCCAACGGCCAAGATGAGA         400

AAAGTCCAAGCACTTCCCATGATGTCTCCGTTCCTCAGGAGTCTCAGGGA         450

GCTTCACCCACTGGCTCGCCTGATGCAGGTGTTTCAGGCTCAAAATATGA         500

TGTGGCTGCCGAGGGTGAAGATGAGGAAAGTGTAAGCGCCTCACAGAAAG         550
                  SL192
CCATCATTTTTAAGCGCTTAAGCAAAGATGCTGTAAAGAAGAAGGCGTGC         600

ACGTTGGCGCAATTCCTGCAGAAGAAGTTTGAGAAGAAAGAGTCCATTTT         650

GAAGGCAGACATGCTGAAGTGTGTCCGCAGAGAGTACAAGCCCTACTTCC         700

CTCAGATCCTCAACAGAACCTCCCAACATTTGGTGGTGGCCTTTGGCGTT         750

GAATTGAAAGAAATGGATTCCAGCGGCGAGTCCTACACCCTTGTCAGCAA         800

GCTAGGCCTCCCCAGTGAAGGAATTCTGAGTGGTGATAATGCGCTGCCGA         850

AGTCGGGTCTCCTGATGTCGCTCCTGGTTGTGATCTTCATGAACGGCAAC         900

TGTGCCACTGAAGAGGAGGTCTGGGAGTTCCTGGGTCTGTTGGGGATATA         950

TGATGGGATCCTGCATTCAATCTATGGGGATGCTCGGAAGATCATTACTG        1000

AAGATTTGGTGCAAGATAAGTACGTGGTTTACCGGCAGGTGTGCAACAGT        1050

GATCCTCCATGCTATGAGTTCCTGTGGGGTCCACGAGCCTATGCTGAAAC        1100

CACCAAGATGAGAGTCCTGCGTGTTTTGGCCGACAGCAGTAACACCAGTC        1150

CCGGTTTATACCCACATCTGTATGAAGACGCTTTGATAGATGAGGTAGAG        1200

AGAGCATTGAGACTGAGAGCTTAA                                 1224
```

Figure 10 **Amino-acid sequence of the putative MAGE-B6 protein (SEQ ID NO: 26)**

```
MPRGHKSKLRTCEKRQETNGQPQGLTGPQATAEKQEESHSSSSSSRACLG          50
DCRRSSDASIPQESQGVSPTGSPDAVVSYSKSDVAANGQDEKSPSTSRDA         100
SVPQESQGASPTGSPDAGVSGSKYDVAANGQDEKSPSTSHDVSVPQESQG         150
ASPTGSPDAGVSGSKYDVAAEGEDEESVSASQKAIIFKRLSKDAVKKAC          200
TLAQFLQKKFEKKESILKADMLKCVRREYKPYFPQILNRTSQHLVVAFGV         250
ELKEMDSSGESYTLVSKLGLPSEGILSGDNALPKSGLLMSLLVVIFMNGN         300
CATEEEVWEFLGLLGIYDGILHSIYGDARKIITEDLVQDKYVVYRQVCNS         350
DPPCYEFLWGPRAYAETTKMRVLRVLADSSNTSPGLYPHLYEDALIDEVE         400
RALRLRA                                                     407
```